SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Meissner, Paul S.
Coleman, Timothy A.

(ii) TITLE OF INVENTION: Human Criptin Growth Factor

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850



(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/393,023
(B) FILING DATE: 09-SEP-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/471,371
(B) FILING DATE: 06-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Marks, Michelle S.
(B) REGISTRATION NUMBER: 41,971
(C) REFERENCE/DOCKET NUMBER: PF200D1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 301-309-8504
(B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA        48
Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
  1               5                  10                  15

TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC        96
Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
            20                  25                  30

GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG       144
Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
         35                  40                  45

TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC       192
Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
     50                  55                  60

GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC       240
Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
 65                  70                  75                  80

GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC       288
Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
                85                  90                  95

TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC       336
Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
            100                 105                 110

TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC       384
Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
        115                 120                 125

GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG       432
Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
    130                 135                 140

GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA       480
Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
145                 150                 155                 160

GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC       528
Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
                165                 170                 175

AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC       576
Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
            180                 185                 190

CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG       624
Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
        195                 200                 205

CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA       672
Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu  *
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
 1               5                  10                  15

Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
            20                  25                  30

Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
        35                  40                  45

Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
    50                  55                  60

Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
65                  70                  75                  80

Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
                85                  90                  95

Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
            100                 105                 110

Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
        115                 120                 125

Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
    130                 135                 140

Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
145                 150                 155                 160

Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
                165                 170                 175

Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
            180                 185                 190

Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
        195                 200                 205

Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu  *
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGGAT CCAATTTGGG AAACAGCTAT CAAAGA

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC 42

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

B1 cont

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT 36

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC 42

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met His Ala Ala Ile Ser Lys Val Phe Glu Leu Gly Leu Val Ala Gly
1 5 10 15

Leu Gly His Gln Glu Phe Ala Arg Pro Ser Arg Gly Tyr Leu Ala Phe
20 25 30

```
Arg Asp Asp Ser Ile Trp Pro Gln Glu Glu Pro Ala Ile Arg Pro Arg
        35                  40                  45

Ser Ser Gln Arg Val Pro Pro Met Gly Ile Gln His Ser Lys Glu Leu
    50                  55                  60

Asn Arg Thr Cys Cys Leu Asn Gly Gly Thr Cys Met Leu Gly Ser Phe
65                  70                  75                  80

Cys Ala Cys Pro Pro Ser Phe Tyr Gly Arg Asn Cys Glu His Asp Val
                85                  90                  95

Arg Lys Glu Asn Cys Gly Ser Val Pro His Asp Thr Trp Leu Pro Lys
            100                 105                 110

Lys Cys Ser Leu Cys Lys Cys Trp His Gly Gln Leu Arg Cys Phe Pro
        115                 120                 125

Gln Ala Phe Leu Pro Gly Cys Asp Gly Leu Val Met Asp Glu His Leu
    130                 135                 140

Val Ala Ser Arg Thr Pro Glu Leu Pro Pro Ser Ala Arg Thr Thr Thr
145                 150                 155                 160

Phe Leu Met Val Gly Ile Cys Leu Ser Ile Gln Ser Tyr Tyr
                165                 170
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B1 (cont.)